

**TABLE S2**

**Estimates of the distribution of fitness effects and the fraction of adaptive substitutions using the simplified LCBN method  
on the dataset restricted to the two-thirds of loci with the highest  $K_A/K_S$  values**

Dataset	Neutrality index ( $\hat{m}_i$ )	$c_{nc}$	$N_{esH}$	$\alpha$
Full dataset				
X chromosome	1.62 (0.57/1.81)	0.022 (0.005/0.046)	9.93 (4.78/infinity)	0.66 (0.31/0.92)
Autosomes	2.51 (1.29/3.40)	-0.003 (-0.018/0.011)	4.38 (2.80/8.36)	1.07 (0.78/1.34)
Restricted by $K_A/K_S$				
X chromosome	0.91 (0.42/1.63)	0.029 (0.005/0.046)	8.81 (3.63/infinity)	0.67 (0.32/0.97)
Autosomes	1.37 (1.18/3.40)	-0.023 (-0.025/0.020)	3.25 (2.06/6.56)	1.07 (0.70/1.32)

95% confidence intervals in parentheses (generated by bootstrapping across genes 1000 times).

Calculations were carried out as described by LOEWE *et al.* (2006).